ENTERED   OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/718,321A

DATE: 07/10/2002 P.6
TIME: 10:44:58

Input Set : D:\Cura-99.app
Output Set: N:\CRF3\07102002\I718321A.raw

```
       4 <110> APPLICANT: Shimkets, Richard A.
       5         Leach, Martin D.
       7 <120> TITLE OF INVENTION: NUCLEIC ACIDS CONTAINING SINGLE NUCLEIC ACID POLYMORPHISMS
AND METHODS OF
       8         USE THEREOF
      10 <130> FILE REFERENCE: 15966-599
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/718,321A
C--> 12 <141> CURRENT FILING DATE: 2002-06-20
      12 <150> PRIOR APPLICATION NUMBER: 60/163,783
      13 <151> PRIOR FILING DATE: 1999-11-24
      15 <160> NUMBER OF SEQ ID NOS: 1468
      17 <170> SOFTWARE: CuraGen Patent Formatter Version 0.9
      19 <210> SEQ ID NO: 1
      20 <211> LENGTH: 51
      21 <212> TYPE: DNA
      22 <213> ORGANISM: Homo sapiens
      24 <220> FEATURE:
      25 <221> NAME/KEY: allele
      26 <222> LOCATION: (26)...(0)
      27 <223> OTHER INFORMATION: single nucleotide polymorphism
      29 <221> NAME/KEY: misc_feature
      30 <222> LOCATION: (0)...(0)
      31 <223> OTHER INFORMATION: Accession number cg43921971
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      37 <211> LENGTH: 51
      38 <212> TYPE: DNA
      39 <213> ORGANISM: Homo sapiens
      41 <220> FEATURE:
      42 <221> NAME/KEY: allele
      43 <222> LOCATION: (26)...(0)
      44 <223> OTHER INFORMATION: single nucleotide polymorphism
      46 <221> NAME/KEY: misc_feature
      47 <222> LOCATION: (0)...(0)
      48 <223> OTHER INFORMATION: Accession number cg43336508
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      54 <211> LENGTH: 50
      55 <212> TYPE: DNA
      56 <213> ORGANISM: Homo sapiens
      58 <220> FEATURE:
      59 <221> NAME/KEY: allele
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Input Set : **D:\Cura-99.app**
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        61 <223> OTHER INFORMATION: single nucleotide polymorphism
        63 <221> NAME/KEY: misc_feature
        64 <222> LOCATION: (25)...(26)
        65 <223> OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
W--> 67 <221> misc_feature
        68 <222> LOCATION: (0)...(0)
        69 <223> OTHER INFORMATION: Accession number cg43314087
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        75 <211> LENGTH: 50
        76 <212> TYPE: DNA
        77 <213> ORGANISM: Homo sapiens
        79 <220> FEATURE:
        80 <221> NAME/KEY: allele
        81 <222> LOCATION: (26)...(0)
        82 <223> OTHER INFORMATION: single nucleotide polymorphism
        84 <221> NAME/KEY: misc_feature
        85 <222> LOCATION: (25)...(26)
        86 <223> OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
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        93 tttgtttttg tttttgtttt tttttaaagg caaagggGtc tgaagagatg        50
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        98 <213> ORGANISM: Homo sapiens
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       101 <221> NAME/KEY: allele
       102 <222> LOCATION: (26)...(0)
       103 <223> OTHER INFORMATION: single nucleotide polymorphism
       105 <221> NAME/KEY: misc_feature
       106 <222> LOCATION: (25)...(26)
       107 <223> OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
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       118 <212> TYPE: DNA
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       121 <220> FEATURE:
       122 <221> NAME/KEY: allele
       123 <222> LOCATION: (26)...(0)
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Input Set : **D:\Cura-99.app**
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       126 <221> NAME/KEY: misc_feature
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       139 <212> TYPE: DNA
       140 <213> ORGANISM: Homo sapiens
       142 <220> FEATURE:
       143 <221> NAME/KEY: allele
       144 <222> LOCATION: (26)...(0)
       145 <223> OTHER INFORMATION: single nucleotide polymorphism
       147 <221> NAME/KEY: misc_feature
       148 <222> LOCATION: (0)...(0)
       149 <223> OTHER INFORMATION: Accession number cg43988460
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       152 taccaaaaaa aaaaaggaaa ggaaaaaaag gggtggcctg acactggtgg c           51
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       156 <212> TYPE: DNA
       157 <213> ORGANISM: Homo sapiens
       159 <220> FEATURE:
       160 <221> NAME/KEY: allele
       161 <222> LOCATION: (26)...(0)
       162 <223> OTHER INFORMATION: single nucleotide polymorphism
       164 <221> NAME/KEY: misc_feature
       165 <222> LOCATION: (25)...(26)
       166 <223> OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
W--> 168 <221> misc_feature
       169 <222> LOCATION: (0)...(0)
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       173 gacacatgtc aggctggggc agcagcactc tgatcagcac caggtcccga            50
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       176 <211> LENGTH: 50
       177 <212> TYPE: DNA
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       180 <220> FEATURE:
       181 <221> NAME/KEY: allele
       182 <222> LOCATION: (26)...(0)
       183 <223> OTHER INFORMATION: single nucleotide polymorphism
       185 <221> NAME/KEY: misc_feature
       186 <222> LOCATION: (25)...(26)
       187 <223> OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
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RAW SEQUENCE LISTING   DATE: 07/10/2002
PATENT APPLICATION: US/09/718,321A   TIME: 10:44:58

            Input Set : D:\Cura-99.app
            Output Set: N:\CRF3\07102002\I718321A.raw

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     190 <222> LOCATION: (0)...(0)
     191 <223> OTHER INFORMATION: Accession number cg43266931
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     197 <211> LENGTH: 50
     198 <212> TYPE: DNA
     199 <213> ORGANISM: Homo sapiens
     201 <220> FEATURE:
     202 <221> NAME/KEY: allele
     203 <222> LOCATION: (26)...(0)
     204 <223> OTHER INFORMATION: single nucleotide polymorphism
     206 <221> NAME/KEY: misc_feature
     207 <222> LOCATION: (25)...(26)
     208 <223> OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
W--> 210 <221> misc_feature
     211 <222> LOCATION: (0)...(0)
     212 <223> OTHER INFORMATION: Accession number cg43321451
W--> 214 <400> 10
     215 gaaggcacac acacacacac acacaagcaa aagctaaatc atcacccgcg        50
     217 <210> SEQ ID NO: 11
     218 <211> LENGTH: 51
     219 <212> TYPE: DNA
     220 <213> ORGANISM: Homo sapiens
     222 <220> FEATURE:
     223 <221> NAME/KEY: allele
     224 <222> LOCATION: (26)...(0)
     225 <223> OTHER INFORMATION: single nucleotide polymorphism
     227 <221> NAME/KEY: misc_feature
     228 <222> LOCATION: (0)...(0)
     229 <223> OTHER INFORMATION: Accession number cg43933757
W--> 231 <400> 11
     232 tcatctccct gcaacctccg cctcccgggt tcaagcgatt cttgtgcctc a      51
     234 <210> SEQ ID NO: 12
     235 <211> LENGTH: 51
     236 <212> TYPE: DNA
     237 <213> ORGANISM: Homo sapiens
     239 <220> FEATURE:
     240 <221> NAME/KEY: allele
     241 <222> LOCATION: (26)...(0)
     242 <223> OTHER INFORMATION: single nucleotide polymorphism
     244 <221> NAME/KEY: misc_feature
     245 <222> LOCATION: (0)...(0)
     246 <223> OTHER INFORMATION: Accession number cg43933757
W--> 248 <400> 12
     249 ccgcctcctg ggttcaagcg attctcgtgc ctcagcctcc caagcagctg g      51
     251 <210> SEQ ID NO: 13
     252 <211> LENGTH: 51
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RAW SEQUENCE LISTING   DATE: 07/10/2002
PATENT APPLICATION: US/09/718,321A   TIME: 10:44:58

Input Set : **D:\Cura-99.app**
Output Set: **N:\CRF3\07102002\I718321A.raw**

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      254 <213> ORGANISM: Homo sapiens
      256 <220> FEATURE:
      257 <221> NAME/KEY: allele
      258 <222> LOCATION: (26)...(0)
      259 <223> OTHER INFORMATION: single nucleotide polymorphism
      261 <221> NAME/KEY: misc_feature
      262 <222> LOCATION: (0)...(0)
      263 <223> OTHER INFORMATION: Accession number cg43933757
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      266 tccaactcct gacctcaggt aatccacctg ccttggcctc ccaaagtgct g        51
      268 <210> SEQ ID NO: 14
      269 <211> LENGTH: 50
      270 <212> TYPE: DNA
      271 <213> ORGANISM: Homo sapiens
      273 <220> FEATURE:
      274 <221> NAME/KEY: allele
      275 <222> LOCATION: (26)...(0)
      276 <223> OTHER INFORMATION: single nucleotide polymorphism
      278 <221> NAME/KEY: misc_feature
      279 <222> LOCATION: (25)...(26)
      280 <223> OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
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      290 <211> LENGTH: 50
      291 <212> TYPE: DNA
      292 <213> ORGANISM: Homo sapiens
      294 <220> FEATURE:
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      296 <222> LOCATION: (26)...(0)
      297 <223> OTHER INFORMATION: single nucleotide polymorphism
      299 <221> NAME/KEY: misc_feature
      300 <222> LOCATION: (25)...(26)
      301 <223> OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
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      310 <210> SEQ ID NO: 16
      311 <211> LENGTH: 51
      312 <212> TYPE: DNA
      313 <213> ORGANISM: Homo sapiens
      315 <220> FEATURE:
      316 <221> NAME/KEY: allele
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/10/2002
PATENT APPLICATION: US/09/718,321A   TIME: 10:44:59

Input Set : D:\Cura-99.app
Output Set: N:\CRF3\07102002\I718321A.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:120; N Pos. 1

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 7

VERIFICATION SUMMARY   DATE: 07/10/2002
PATENT APPLICATION: **US/09/718,321A**   TIME: 10:44:59

Input Set : **D:\Cura-99.app**
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```
L:12  M:270 C: Current Application Number differs, Replaced Current Application No
L:12  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:33  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:50  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:67  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:71  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:88  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:92  M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:109 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:113 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:130 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:134 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:151 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:168 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:172 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:189 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
L:193 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
L:210 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:10
L:214 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:10
L:231 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:248 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:12
L:265 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:13
L:282 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:14
L:286 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:14
L:303 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:307 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:324 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:16
L:341 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:17
L:358 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:18
L:375 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:392 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:20
L:396 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:20
L:413 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:21
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L:434 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:22
L:451 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:23
L:468 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:24
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L:502 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26
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L:523 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:27
L:540 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:28
L:557 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:29
L:574 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:30
L:591 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:31
L:608 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:32
L:625 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:33
L:642 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:34
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VERIFICATION SUMMARY   DATE: 07/10/2002
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Input Set : **D:\Cura-99.app**
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L:730 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:39
L:765 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:41
L:769 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:41
L:2186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:120 after pos.:0
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